

SEQUENCE LISTING

Sab
a' />

<110> National Institute of Agrobiological Sciences

<120> Sodium/Proton antiporter gene

<130> MOA-006PCT

<150> JP 1998-365604

<151> 1998-12-22

<160> 2

<170> PatentIn Ver. 2.0

<210> 1

<211> 2330

<212> DNA

<213> Oryza sativa

<220>

<221> CDS

<222> (297)..(1901)

<400> 1

gagaagagag tttttagcg agctcgcg aatgcgaagc caaccgagag aggtctcgat 60

acccaaatccc gatttctcaa cctgaatccc ccccccacgt tcctcgttt aatctgttcg 120

tctgcgaatc gaattctttg ttttttttc tctaattttt ccggaaatttgcgaattttagg 180

cattcaccaa cgagcaagag gggagtggtt aagctccgca tcttgcggcg 240

gaaatctcgc tctcttcct gcggtggttgc gccggagaag tcgcccgg tgaggc atg 299

Met

1

ggg atg gag gtg gcg gcg cgg ctg ggg gct ctg tac acg acc tcc 347

Gly Met Glu Val Ala Ala Ala Arg Leu Gly Ala Leu Tyr Thr Thr Ser

5

10

15

gac tac gcg tcg gtg gtg tcc atc aac ctg ttc gtc gcg ctg ctg tgc 395

Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu Cys

20

25

30

gcc tgc atc gtc ctc ggc cac ctc ctg gag gag aat cgc tgg gtc aat 443

Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val Asn

35

40

45

gag tcc atc acc gcg ctc atc atc ggg ctc tgc acc ggc gtg gtg atc 491

Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val Ile

50

55

60

65

ttg ctg atg acc aaa ggg aag agc tcg cac tta ttc gtc ttc agt gag 539
 Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser Glu

70

75

80

gat ctc ttc ttc atc tac ctc ctc cct ccg atc atc ttc aat gca ggt 587
 Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly

85

90

95

ttt cag gta aag aaa aag caa ttc ttc cgg aat ttc atg acg atc aca 635
 Phe Gln Val Lys Lys Gln Phe Phe Arg Asn Phe Met Thr Ile Thr

100

105

110

tta ttt gga gcc gtc ggg aca atg ata tcc ttt ttc aca ata tct att 683
 Leu Phe Gly Ala Val Gly Thr Met Ile Ser Phe Phe Thr Ile Ser Ile

115

120

125

gct gcc att gca ata ttc agc aga atg aac att gga acg ctg gat gta 731
 Ala Ala Ile Ala Ile Phe Ser Arg Met Asn Ile Gly Thr Leu Asp Val

130

135

140

145

gga gat ttt ctt gca att gga gcc atc ttt tct gcg aca gat tct gtc 779
 Gly Asp Phe Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp Ser Val

150

155

160

DRAFT DRAFT DRAFT DRAFT

tgc aca ttg cag gtc ctc aat cag gat gag aca ccc ttt ttg tac agt 827
 tgc aca ttg cag gtc ctc aat cag gat gag aca ccc ttt ttg tac agt 827
 Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Phe Leu Tyr Ser
 165 170 175

ctg gta ttc ggt gaa ggt gtt gtg aac gat gct aca tca att gtg ctt 875
 Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Ile Val Leu
 180 185 190

ttc aac gca cta cag aac ttt gat ctt gtc cac ata gat gcg gct gtc 923
 ttc aac gca cta cag aac ttt gat ctt gtc cac ata gat gcg gct gtc 923
 Phe Asn Ala Leu Gln Asn Phe Asp Leu Val His Ile Asp Ala Ala Val
 195 200 205

gtt ctg aaa ttc ttg ggg aac ttc ttt tat tta ttt ttg tcg agc acc 971
 Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser Thr
 210 215 220 225

ttc ctt gga gta ttt gct gga ttg ctc agt gca tac ata atc aag aag 1019
 ttc ctt gga gta ttt gct gga ttg ctc agt gca tac ata atc aag aag 1019
 Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys Lys
 230 235 240

cta tac att gga agg cat tct act gac cgt gag gtt gcc ctt atg atg 1067
 cta tac att gga agg cat tct act gac cgt gag gtt gcc ctt atg atg 1067
 Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met Met
 245 250 255

ctc atg gct tac ctt tca tat atg ctg gct gag ttt cta gat ttg agc 1115
 ctc atg gct tac ctt tca tat atg ctg gct gag ttt cta gat ttg agc 1115
 Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu Ser

260 265

270

ggc att ctc acc gta ttc ttc tgt ggt att gta atg tca cat tac act 1163
 Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr

275 280

285

tgg cat aac gtc aca gag agt tca aga gtt aca aca aag cac gca ttt 1211
 Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala Phe

290 295

300

305

gca act ctg tcc ttc att gct gag act ttt ctc ttc ctg tat gtt ggg 1259
 Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val Gly

310 315

320

atg gat gca ttg gat att gaa aaa tgg gag ttt gcc agt gac aga cct 1307
 Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg Pro

325 330

335

ggc aaa tcc att ggg ata agc tca att ttg cta gga ttg gtt ctg att 1355
 Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu Ile

340 345

350

gga aga gct gct ttt gta ttc ccg ctg tcg ttc ttg tcg aac cta aca 1403
 Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu Thr

355 360

365

aag aag gca ccg aat gaa aaa ata acc tgg aga cag caa gtt gla ata 1451
 Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val Ile
 370 375 380 385

tgg tgg gct ggg ctg atg aga gga gct gtg tcg att gct ctt gct tac 1499
 Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala Tyr
 390 395 400

aat aag ttt aca aga tct ggc cat act cag ctg cac ggc aat gca ata 1547
 Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala Ile
 405 410 415

atg atc acc agc acc atc act gtc gtt ctt ttt agc act atg gta ttt 1595
 Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val Phe
 420 425 430

ggg atg atg aca aag cca ttg atc agg ctg ctg cta ccg gcc tca ggc 1643
 Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Leu Pro Ala Ser Gly
 435 440 445

cat cct gtc acc tct gag cct tca cca aag tcc ctg cat tct cct 1691
 His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser Pro
 450 455 460 465

ctc ctg aca agc atg caa ggt tct gac ctc gag agt aca acc aac att 1739
 Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn Ile

470

475

480

gtg agg cct tcc agc ctc cgg atg ctc ctc acc aag ccg acc cac act 1787
 Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His Thr

485

490

495

gtc cac tac tac tgg cgc aag ttc gac gac gcg ctg atg cga ccg atg 1835
 Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro Met

500

505

510

ttt ggc ggg cgc ggg ttc gtg ccc ttc tcc cct gga tca cca acc gag 1883
 Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr Glu

515

520

525

cag agc cat gga gga aga tgaacaglgc aaagaaaatga gaatggaaatg 1931
 Gln Ser His Gly Gly Arg

530

535

gtttagatgagg agaaatcatg taaaatgtga cagcaaaaga gagaaggcaa gttttgggtt 1991

tgttagatgtt ggctgtgtgtt aatgagttgt ttagatgtgcc tataatcttc agaacttcag 2051

atggtgcctc accaaggccct aagagccagg aggacccttc gataatggtt cggatgatt 2111

ggtttttttc gtcaggatga acccttagtga gtcacacagg gtcgtgtgtt ccgacaacct 2171

gtaaatttt tagattaaca gccccatttg tacctgtcta ccaatctttag ttggcggttg 2231

ttctttccta gttgccaccc tgcatglaaa algaatatict ccgccaaaat agattttgtl 2291

gtataataat ttgcgttgtt tgaaaaaaaaaaaaaaa aaaaaaaaaa 2330

〈210〉 2

211 > 535

<212> PRT

<213> *Oryza sativa*

<400> 2

Met Gly Met Glu Val Ala Ala Ala Arg Leu Gly Ala Leu Tyr Thr Thr

1

5

10

15

Ser Asp Tyr Ala Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Leu

20

25

30

Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val

35

40

45

Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val

50

55

60

Ile Leu Leu Met Thr Lys Gly Lys Ser Ser His Leu Phe Val Phe Ser

65	70	75	80
----	----	----	----

Glu	Asp	Leu	Phe	Phe	Ile	Tyr	Leu	Leu	Pro	Pro	Ile	Phe	Asn	Ala
85									90				95	

Gly	Phe	Gln	Val	Lys	Lys	Gln	Phe	Phe	Arg	Asn	Phe	Met	Thr	Ile
100							105					110		

Thr	Leu	Phe	Gly	Ala	Val	Gly	Thr	Met	Ile	Ser	Phe	Thr	Ile	Ser
115							120					125		

Ile	Ala	Ala	Ile	Ala	Ile	Phe	Ser	Arg	Met	Asn	Ile	Gly	Thr	Leu	Asp
130						135						140			

Val	Gly	Asp	Phe	Leu	Ala	Ile	Gly	Ala	Ile	Phe	Ser	Ala	Thr	Asp	Ser
145						150				155			160		

Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Asp	Glu	Thr	Pro	Phe	Leu	Tyr
165							170					175			

Ser	Leu	Val	Phe	Gly	Glu	Gly	Val	Val	Asn	Asp	Ala	Thr	Ser	Ile	Val
180							185					190			

Leu	Phe	Asn	Ala	Leu	Gln	Asn	Phe	Asp	Leu	Val	His	Ile	Asp	Ala	Ala
195							200					205			

Val Val Leu Lys Phe Leu Gly Asn Phe Phe Tyr Leu Phe Leu Ser Ser

210

215

220

Thr Phe Leu Gly Val Phe Ala Gly Leu Leu Ser Ala Tyr Ile Ile Lys

225

230

235

240

Lys Leu Tyr Ile Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met

245

250

255

Met Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Leu Asp Leu

260

265

270

Ser Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr

275

280

285

Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Ala

290

295

300

Phe Ala Thr Leu Ser Phe Ile Ala Glu Thr Phe Leu Phe Leu Tyr Val

305

310

315

320

Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Glu Phe Ala Ser Asp Arg

325

330

335

Pro Gly Lys Ser Ile Gly Ile Ser Ser Ile Leu Leu Gly Leu Val Leu

340

345

350

Ile Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu

355

360

365

Thr Lys Lys Ala Pro Asn Glu Lys Ile Thr Trp Arg Gln Gln Val Val

370

375

380

Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala

385

390

395

400

Tyr Asn Lys Phe Thr Arg Ser Gly His Thr Gln Leu His Gly Asn Ala

405

410

415

Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Met Val

420

425

430

Phe Gly Met Met Thr Lys Pro Leu Ile Arg Leu Leu Pro Ala Ser

435

440

445

Gly His Pro Val Thr Ser Glu Pro Ser Ser Pro Lys Ser Leu His Ser

450

455

460

Pro Leu Leu Thr Ser Met Gln Gly Ser Asp Leu Glu Ser Thr Thr Asn

465

470

475

480

Ile Val Arg Pro Ser Ser Leu Arg Met Leu Leu Thr Lys Pro Thr His

485

490

495

Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asp Ala Leu Met Arg Pro

500

505

510

Met Phe Gly Gly Arg Gly Phe Val Pro Phe Ser Pro Gly Ser Pro Thr

515

520

525

Glu Gln Ser His Gly Gly Arg

530

535

DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT DRAFT